AMENDMENTS TO THE CLAIMS:

The following is a complete listing of the claims, and replaces all earlier listings and versions:

1-45. (canceled)

46. (new) A method for screening a test compound for the ability to induce anergy in T cells, said method comprising the steps of:

a) contacting a first sample of T cells with the test compound; and

b) detecting the absence or presence of NFAT signaling in the first sample of T cells,

wherein the presence of NFAT signaling indicates the ability of the test compound to induce anergy in T cells.

47. (new) The method of claim 46, wherein said detecting step comprises:

a) determining a first set of expression levels in the first sample of T cells for a panel of anergy marker proteins encoded by anergy markers listed in Group I or Group II or Group III or Group IV; and

b) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from a second sample of T cells that have been activated,

wherein the presence of NFAT signaling is detected when the first set of expression levels is higher than the second set of expression levels.

48. (new) The method of claim 46, wherein said detecting step comprises:

a) determining a first set of expression levels in the first sample of T cells for a panel of anergy marker proteins, wherein the anergy markers encoding the panel of anergy

marker proteins are selected from the group consisting of GRG4, jumonji, RPTPσ, PTP-1B, RPTPκ, GBP-3, caspase-3, SOCS-2, DAGKα, LDHAα, CD98, 4-IBB-L, and FasL; and

b) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from a second sample of T cells that have been activated,

wherein the presence of NFAT signaling is detected when the first set of expression levels is higher than the second set of expression levels.

49. (new) The method of claim 46, wherein said detecting step comprises:

a) determining a first set of expression levels in the first sample of T cells for a panel of anergy marker proteins, wherein the anergy markers encoding the panel of anergy marker proteins comprise GRG4, ikaros, jumonji, RPTPσ, PTP-1B, RPTPκ, GBP-3, RGS-2, caspase-3, SOCS-2, DAGKα, LDHAα, CD98, 4-IBB-L, and FasL; and

b) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from a second sample of T cells that have been activated,

wherein the presence of NFAT signaling is detected when the first set of expression levels is higher than the second set of expression levels.

50. (new) The method of claim 47, wherein the panel of anergy marker proteins comprises transcription proteins, proteins involved in G-protein signaling, tyrosine phosphatases, proteins involved in proteolytic pathways, cell-surface receptor proteins, and metabolic and signaling enzymes.

51. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises transcription proteins comprising GRG4, ikaros, and jumonji.

52. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises proteins involved in G-protein signaling comprising GBP-3 and RGS-2.

53. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises tyrosine phosphatases comprising RPTPσ, PTP-1B, and RPTPκ.

54. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises proteins involved in proteolytic pathways comprising caspase-3 and SOCS-2.

55. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises cell surface receptor proteins comprising CD98, 4-IBB-L, and FasL.

56. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises metabolic and signaling enzymes comprising DAGKα and LDHAα.

57. (new) The method of claim 50, wherein the panel of anergy marker proteins comprises jumonji, RPTPκ, GBP-3, caspase-3, DAGKα, and FasL.

58. (new) The method of claim 46, wherein the method of screening is high-throughput screening.

59. (new) The method of claim 46, wherein the test compound is a small molecule.

60. (new) The method of claim 46, wherein the test compound is from a library selected from the group consisting of spatially addressable parallel solid phase libraries, spatially addressable parallel solution phase libraries, synthetic libraries made from

deconvolution, synthetic libraries made by 'one-bead one-compound' methods, and synthetic libraries made by affinity chromatography selection.

61. (new) The method of claim 46, wherein the test compound is a bioactive agent selected from the group consisting of naturally occurring compounds, biomolecules, proteins, peptides, oligopeptides, polysaccharides, nucleotides and polynucleotides.

62. (new) A method for screening a test compound for the ability to reduce an unwanted immune response, said method comprising the steps of:

a) contacting a first sample of T cells isolated from a patient suffering from the unwanted immune response with the test compound; and

b) detecting the absence or presence of NFAT signaling in the first sample of T cells,

wherein the presence of NFAT signaling indicates the ability of the test compound to reduce the unwanted immune response.

63. (new) The method of claim 62, wherein said detecting step comprises:

a) determining a first set of expression levels in the first sample of T cells for a panel of anergy marker proteins encoded by anergy markers listed in Group I or Group II or Group III or Group IV; and

b) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from a second sample of T cells isolated from the patient that have been activated,

wherein the presence of NFAT signaling is detected when the first set of expression levels is higher than the second set of expression levels.

64. (new) The method of claim 62, wherein the unwanted immune response results in an immune disorder selected from the group consisting of diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis, encephalomyelitis, diabetes, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis, allergy, asthma, allergic asthma, psoriasis, Sjogren's syndrome, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative colitis, discoid lupus erythematosus, scleroderma, vaginitis, proctitis, drug eruptions, leprosy reversal reactions, erythema nodosum leprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotizing hemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anemia, pure red cell anemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis, uveitis posterior, and interstitial lung fibrosis.

65. (new) The method of claim 62, wherein the unwanted immune response results in an immune disorder selected from the group consisting of transplant rejection and graft-versus-host disease.

66. (new) The method of claim 63, wherein the panel of anergy marker proteins comprises transcription proteins, proteins involved in G-protein signaling, tyrosine phosphatases, proteins involved in proteolytic pathways, cell-surface receptor proteins, and metabolic and signaling enzymes.

67. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises transcription proteins comprising GRG4, ikaros, and jumonji.

68. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises proteins involved in G-protein signaling comprising GBP-3 and RGS-2.

69. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises tyrosine phosphatases comprising RPTPσ, PTP-1B, and RPTPκ.

70. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises proteins involved in proteolytic pathways comprising caspase-3 and SOCS-2.

71. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises cell surface receptor proteins comprising CD98, 4-IBB-L, and FasL.

72. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises metabolic and signaling enzymes comprising DAGKα and LDHAα.

73. (new) The method of claim 66, wherein the panel of anergy marker proteins comprises jumonji, RPTPκ, GBP-3, caspase-3, DAGKα, and FasL.

74. (new) A method for screening a test compound for the ability to heighten immune surveillance, said method comprising the steps of:

a) contacting a first sample of T cells isolated from a patient in need of heightened immune surveillance with the test compound; and

b) detecting the absence or presence of NFAT signaling in the first sample of T cells,

wherein the absence of NFAT signaling indicates the ability of the test compound to heighten immune surveillance.

75. (new) The method of claim 74, wherein said detecting step comprises:

a) determining a first set of expression levels in the first sample of T cells for a panel of anergy marker proteins encoded by anergy markers listed in Group I or Group II or Group III or Group IV; and

b) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from a second sample of T cells subject to anergy induction,

wherein the absence of NFAT signaling is detected when the first set of expression levels is lower than the second set of expression levels.

76. (new) The method of claim 74, wherein the patient in need of heightened immune surveillance is suffering from cancer, or a viral, bacterial or parasitic infection.

77. (new) The method of claim 76, wherein the cancer is selected from the group consisting of lung cancer, breast cancer, lymphoid cancer, gastrointestinal cancer, genitourinary tract cancer, pharynx cancer, colon cancer, renal cell carcinoma, prostate cancer, testicular cancer, non-small cell carcinoma of the lung, small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, pancreatic cancer, ovarian cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinoma, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, cervical cancer, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma,

pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, and retinoblastoma.

78. (new) A method of monitoring the effectiveness of a treatment for a patient suffering from an unwanted immune response, the method comprising:

a) isolating a first sample of T cells from the patient;

b) determining a first set of expression levels in the first sample of T cells for a panel of anergy markers proteins encoded by anergy markers listed in Group I or Group II or Group III or Group IV;

c) treating the patient;

d) isolating a second sample of T cells from the patient; and

e) comparing the first set of expression levels with a second set of expression levels for the panel of anergy marker proteins, said second set of expression levels determined from the second sample of T cells,

wherein the treatment is determined to be effective when the first set of expression levels is lower than the second set of expression levels.